Validated By CRFValidator v 1.0.2

Application No: 10532681 Version No: 1.0

Input Set:

Output Set:

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Finished: 2007-08-13 15:05:08.556
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 300 ms
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Total Errors: 0
No. of SeqIDs Defined: 22
Actual SeqID Count: 22

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SEQUENCE LISTING

<110> LUKYANOV, SERGI A
SHAGIN, DMITRY A
YANUSHEVICH, YURY G

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<140> 10532681
<141> 2007-08-13

<150> 10/532,681
<151> 2005-04-26

<160> 22

<170> PatentIn version 3.3

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gtaccagttc catggtcaac tttagtaaca acacttactt atggtgcaca atgcttcgcc 240

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gagcgtacaa tcacatttga aggggacgga gtatttaaaa ctcgcgctga agttacattt 360

gaaaacggat ctgtttataa ccgagtcaaa cttaatggac aaggatttaa gaaagacgga 420

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gatcacaggg ataacatgag cttggttgaa accgtacggg ctgtggattg cagaaaaaca 720

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<211> 234
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<213> Phialidium sp

<400> 2

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
            20                  25                  30


Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
        35                  40                  45


Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50                  55                  60


Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70                  75                  80


Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
                85                  90                  95


Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
            100                 105                 110


Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
        115                 120                 125


Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130                 135                 140


Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160


Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
                165                 170                 175


Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190


Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
        195                 200                 205
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Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

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<212> DNA
<213> Artificial

<220>
<223> phiYFP-Y1 mutant of the phiYFP

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240

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tctgctttca aaattatgca tgagattact ggatcaaaag gagacttcat tgttgcagac 540

cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600

atgacatacc atgtcactct cagcaaagat gttactgatc acagggataa catgagcttg 660

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<210> 4
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<212> PRT
<213> Artificial

<220>
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<400> 4

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1 5 10 15

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
            20                  25                  30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
        35                  40                  45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50                  55                  60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70                  75                  80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
                85                  90                  95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
            100                 105                 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
        115                 120                 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130                 135                 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser
        195                 200                 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
    210                 215                 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225                 230
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<212> DNA
<213> Artificial

<220>
<223> phiYFP-M0 mutant of the phiYFP

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240

ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300

gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360

gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa 420

ttcaatttca cacctcattg tctttacatt tggggagatc aggctaatca tggtttgaag 480

tctgctttca aaattcgcca tgagattact ggatcaaaag gagacttcat tgttgcagac 540

cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga aaaccatcat 600

atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg 660

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<210> 6
<211> 234
<212> PRT
<213> Artificial

<220>
<223> phiYFP-M0 mutant of the phiYFP

<400> 6

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

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Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70                  75                  80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
                85                  90                  95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
            100                 105                 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
        115                 120                 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130                 135                 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160

Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190

Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
        195                 200                 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
    210                 215                 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225                 230
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<210> 7
<211> 705
<212> DNA
<213> Artificial

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<223> phiYFP-M1 mutant of the phiYFP

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta    180

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat    240

ttctacaaga gttgcatgcc tgatggctat gtgcaggagc gtacaatcac atttgaaggg    300

gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga    360

gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa    420

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tctgctttca aaatttgcca tgagattact ggatcaaaag gagacttcat tgttgcagac    540

cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat    600

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Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1               5                  10                  15


Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
            20                  25                  30


Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
        35                  40                  45


Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50                  55                  60


Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70                  75                  80


Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
                85                  90                  95
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Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
            100                 105                 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
        115                 120                 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130                 135                 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
        195                 200                 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
    210                 215                 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225                 230
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<210> 9
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<220>
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aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg    180

gtgaccaccc tgacctacgg cgcccagtgc ttcgccaagt acggccccga gctgaaggat    240

ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc    300

gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc    360
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ttcaatttca ccccccactg cctgtacatc tggggcgatc aggccaatca cggcctgaag 480

agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat 540

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<212> PRT
<213> Artificial

<220>
<223> humanized version of the phiYFP-M1

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20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

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Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
        195                 200                 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
    210                 215                 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225                 230
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<212> DNA
<213> Anthomedusae species

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gcaatgacag aaacatttca gaaaaaattg ccatataagt tagaattgga tggagatgtt    240

gatgggcaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tggtgtaatt    300

gaaggaaaat atgtttgtac agaaggagaa gttcctattt catgggtttc gctcatcacc    360

tcattaagtt atggtgcgaa atgttttgtt cgatatccaa atgaaataaa tgatttttc     420

aaaagtactt ttccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgatggt    480

gttttagaaa cagcagctaa aattactatg gaaagtggtg caatagtgaa tagaataaat    540

gtgaaaggca caggcttcga taaagatggt catgtatgcc aaaaaaatct tgaatcctcc    600

cctccttcga caacatatgt tgttcccgag ggagaaggta ttcgaatcat ctatagaaac    660
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ctttcaacag atccagaaga aaataaagat catattatca tcaaagaaac caactgcgca 840

tttgacgctg atttttctta agatttccga tttgcatcaa gattgaaaaa ctaaataaag 900

ataggtaaaa aaaatatgtc tttgatgtta catacagtat tgatataagc ttcaaagaaa 960

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<213> Anthomedusae species

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